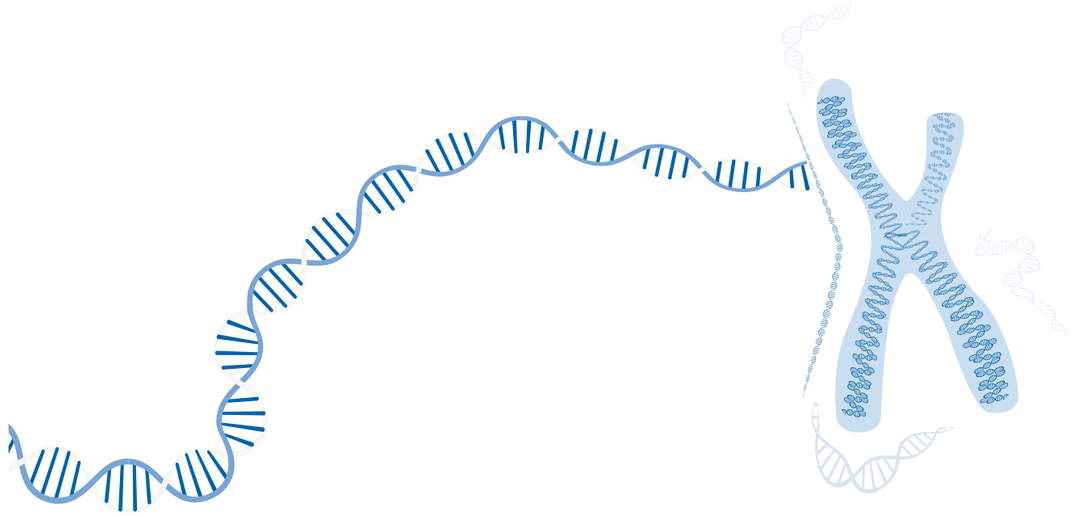
QIAGEN

# Guide to high-molecular-weight DNA extraction and long-read sequencing

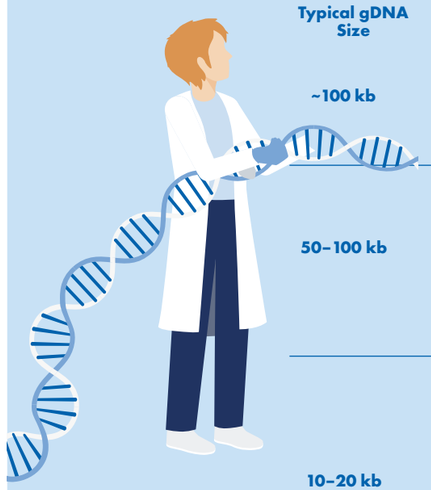
Sample to Insight

# Looking for the right high-molecular-weight genomic DNA kit for long-read sequencing?

Long-read sequencing using PacBio® and Oxford Nanopore Technologies® generate extensive reads for complex genomic studies but it is sensitive to DNA quality and integrity, requiring high-quality, contaminant-free genomic DNA (gDNA). Sample preparation challenges include avoiding DNA contamination, degradation, or shearing to ensure accurate sequencing results. To address these, we offer sample preparation kits for high-molecular-weight (HMW) gDNA samples designed to reduce costs and processing times while maintaining DNA quality and integrity.



**Follow these 3 steps to find the right kit for you:**



**1 What's the length of the genomic DNA?**

**2 What's your sample type and input amount?**

**3 Select the kit with your preferred method of purification**

| Typical gDNA Size | Soil | Stool | Bacteria | Yeast | Cells | Tissue | Blood | Method | Product |
|---|---|---|---|---|---|---|---|---|---|
| ~100 kb | | | | | up to 5 x $10^7$ | 200 mg | 200 µL – 10 mL | Precipitation | Puregene® Kits |
| | | | | | | | 8.5 mL | Precipitation | PAXgene® Blood DNA Kit |
| 50–100 kb | | | 2.2 x $10^{10}$–1 x $10^{11}$ | 7 x$10^9$–3.5 x $10^{10}$ | 2 x$10^7$–1 x $10^8$ | 100–400 mg | 1–20 mL | Anion exchange | QIAGEN® Genomic-tips (only Midi & Maxi) |
| | | | 2.2 x $10^{10}$–1 x $10^{11}$ | 7 x$10^9$–3.5 x $10^{10}$ | 2 x$10^7$–1 x $10^8$ | 100–400 mg | 1–20 mL | Anion exchange | QIAGEN Blood & Cell Culture DNA Kit |
| | | | 2 x $10^9$ | | | up to 25 mg | 200 µL | Beads | MagAttract® HMW DNA Kit |
| 10–20 kb | | | | | | | 200 µL | Spin column | QIAamp® DNA Blood Mini Kit |
| | | | | | 5 x $10^6$ | up to 25 mg | | Spin column | QIAamp DNA Mini Kit |
| | | | | | up to 5 x $10^6$ | up to 25 mg | 100 µL | Spin column | DNeasy® Blood & Tissue Kits |
| | | up to 250 mg | | | | | | Spin column | QIAamp PowerFecal® Pro DNA Kit |
| | up to 250 mg | | | | | | | Spin column | DNeasy PowerSoil® Pro Kit |
| | up to 10 g | | | | | | | Spin column | DNeasy PowerMax® Soil Kit |

**Scan this QR code to learn more about our HMW gDNA extraction kits**

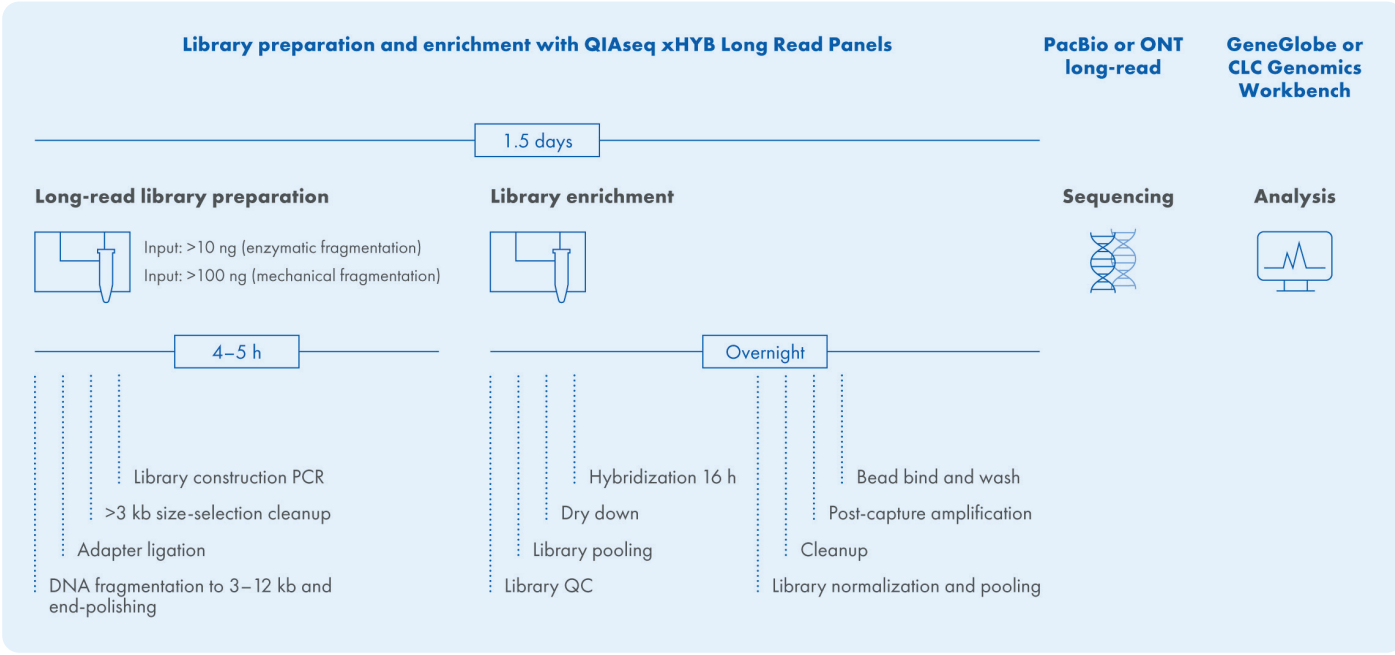
# Play the long game in genomics powered by long reads

With high molecular weight DNA in hand, it's crucial to maintain that integrity throughout the library preparation process to fully realize the benefits of long-read sequencing technologies.

**QIAseq® xHYB Long Read Panels** deliver the resolution you need to tackle the most complex genomic regions using the power of long-read sequencing.

- Complete, uniform coverage with hybrid capture-based target enrichment
- High sensitivity and specificity for accurate variant detection
- Compatible with long-read sequencing for accurate variant calling and phasing
- Flexible and customizable to match diverse research needs and budgets
- Compatible with PacBio (Revio and Vega long-read systems) and ONT long-read systems

# Long-read NGS library preparation and target enrichment workflow




**HLA Typing Panel**

Comprehensive panel design covers all 18 HLA class I and II genes, including introns and UTRs, enabling high-resolution 4-field haplotyping

**Hereditary Cancer Panel**

Targets over 1000 gross deletions, duplications, insertions and complex rearrangements linked to a wide range of cancer types

**Custom Panel**

Fully customizable panel design targets your specific regions of interest, enables integration with existing QIAseq xHYB long-read or custom panels and boosts coverage with additional probes – no ROI limits

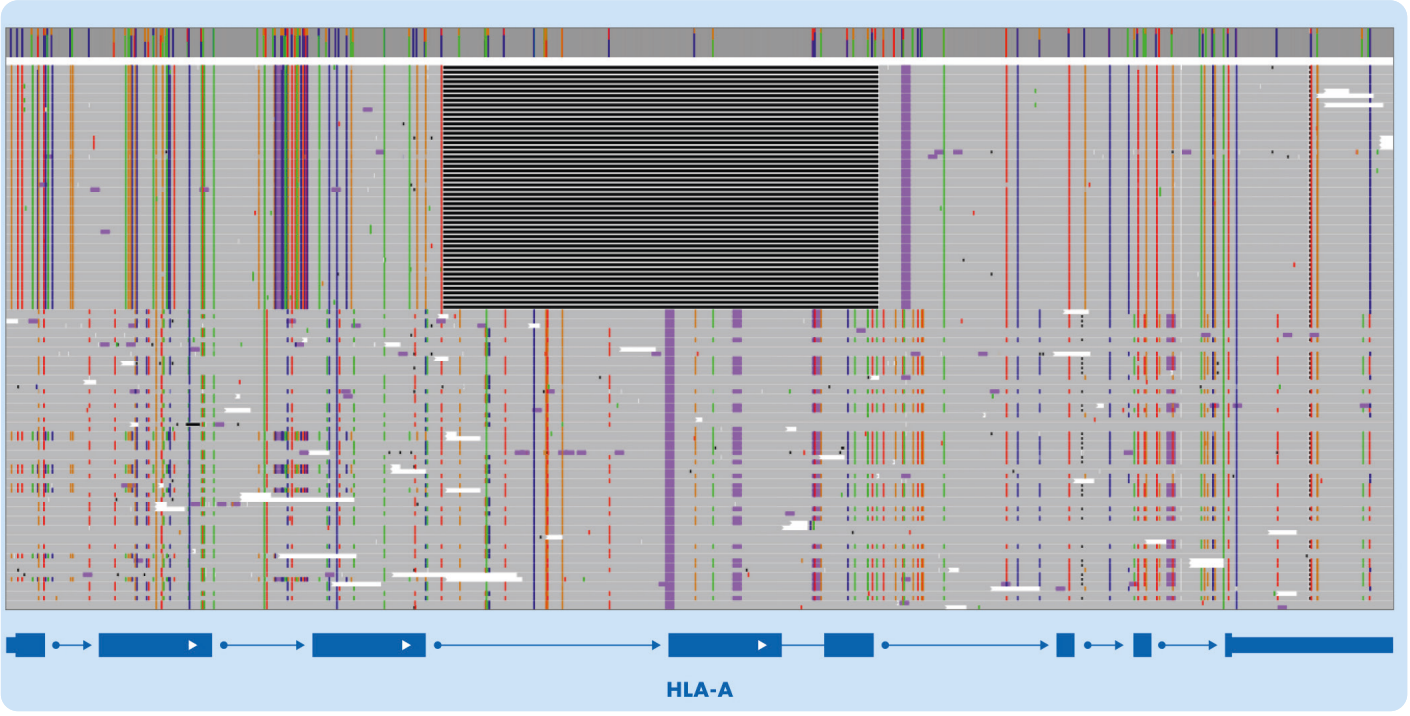



**Figure 1: Long reads generated using the QIAseq xHYB Long Read HLA Typing Panel span the HLA-A gene without assembly, simplifying haplotyping.** Here, we demonstrate the long reads that span the full length of the HLA-A gene, eliminating the need for complex assembly and simplifying the haplotyping process. Visualized read stacks across the gene clearly show heterozygous polymorphisms, with colored markers indicating roughly equal representation of non-reference bases – consistent with the gene's natural allelic diversity.

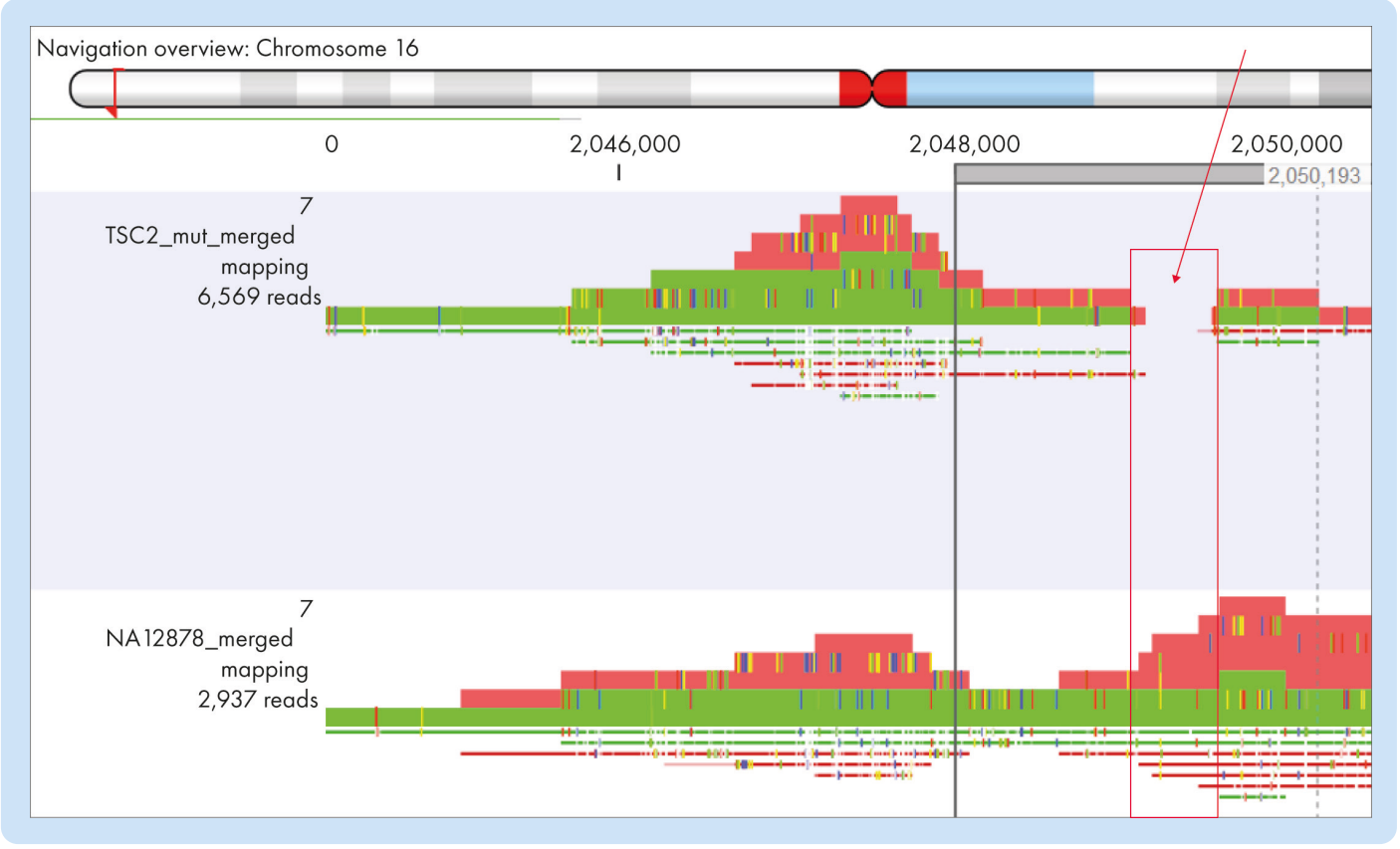



**Figure 2: QIAseq xHYB Long Read Hereditary Cancer Panel successfully detects TSC2 deletion after exon 1 through long reads and contiguous mapping.** The QIAseq xHYB Long Read Hereditary Cancer Panel accurately identifies a large TSC2 deletion in sample NA04520, a structural variant often challenging for short-read methods. The image displays long-read mapping data generated using CLC Genomics Workbench, comparing Coriell reference DNA NA04520 from an affected individual with benchmark reference DNA NA12878. The zoomed-in view of the 5' end of the TSC2 gene clearly shows a 430 bp deletion in NA04520 (indicated by the red arrow and coverage gap).

# Applications

### Repeat expansion disorder analysis

Precisely characterize repeat expansions in neurological and genetic disorders

### Phasing of genetic variants

Determine haplotype structures of genomic variants for critical insights into inheritance patterns and allele-specific expression

### HLA typing

Resolve polymorphic HLA regions for accurate genotyping in immunogenomics and transplantation

### Structural variant detection

Accurately detect large-scale genomic alterations for cancer, genetic disease and evolutionary research

### Data analysis

The GeneGlobe® Data Analysis portal offers simplified downstream data analysis for HLA haplotyping. The QIAGEN® CLC Genomics Workbench is used to detect large structural variants in hereditary cancers.

To learn more about the long-read sequencing panel, visit **https://www.qiagen.com/qiaseq-long-read-seq**

Visit our **Genomic DNA Resource Center for High-Molecular-Weight DNA** and advance your exploration of long-read sequencing.

The products mentioned here are intended for molecular biology applications. These products are not intended for the diagnosis, prevention, or treatment of a disease.

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